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Range: from begin to end Features: ☐ SNP

☐ 1: NP_059122. Reports nucleoporin 54kDa...[gi:26051237]

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LOCUS NP_059122 507 aa linear PRI 11-MAY-2008
 DEFINITION nucleoporin 54kDa [Homo sapiens].
 ACCESSION NP_059122
 VERSION NP_059122.2 GI:26051237
 DBSOURCE REFSEQ: accession [NM_017426.2](#)
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM [Homo sapiens](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 507)
 AUTHORS Le Rouzic,E., Mousnier,A., Rustum,C., Stutz,F., Hallberg,E.,
 Dargemont,C. and Benichou,S.
 TITLE Docking of HIV-1 Vpr to the nuclear envelope is mediated by the
 interaction with the nucleoporin hCG1
 JOURNAL J. Biol. Chem. 277 (47), 45091-45098 (2002)
 PUBMED [12228227](#)

REFERENCE 2 (residues 1 to 507)
 AUTHORS Hu,R.M., Han,Z.G., Song,H.D., Peng,Y.D., Huang,Q.H., Ren,S.X.,
 Gu,Y.J., Huang,C.H., Li,Y.B., Jiang,C.L., Fu,G., Zhang,Q.H.,
 Gu,B.W., Dai,M., Mao,Y.F., Gao,G.F., Rong,R., Ye,M., Zhou,J.,
 Xu,S.H., Gu,J., Shi,J.X., Jin,W.R., Zhang,C.K., Wu,T.M.,
 Huang,G.Y., Chen,Z., Chen,M.D. and Chen,J.L.
 TITLE Gene expression profiling in the human
 hypothalamus-pituitary-adrenal axis and full-length cDNA cloning
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9543-9548 (2000)
 PUBMED [10931946](#)

REFERENCE 3 (residues 1 to 507)
 AUTHORS Stoffler,D., Fahrenkrog,B. and Aeby,U.
 TITLE The nuclear pore complex: from molecular architecture to functional
 dynamics
 JOURNAL Curr. Opin. Cell Biol. 11 (3), 391-401 (1999)
 PUBMED [10395558](#)
 REMARK Review article

REFERENCE 4 (residues 1 to 507)
 AUTHORS Bodoor,K., Shaikh,S., Enarson,P., Chowdhury,S., Salina,D.,
 Raharjo,W.H. and Burke,B.
 TITLE Function and assembly of nuclear pore complex proteins
 JOURNAL Biochem. Cell Biol. 77 (4), 321-329 (1999)
 PUBMED [10546895](#)
 REMARK Review article

REFERENCE 5 (residues 1 to 507)
 AUTHORS Popov,S., Rexach,M., Ratner,L., Blobel,G. and Bukrinsky,M.
 TITLE Viral protein R regulates docking of the HIV-1 preintegration

complex to the nuclear pore complex
 JOURNAL J. Biol. Chem. 273 (21), 13347-13352 (1998)
 PUBMED [9582382](#)
 REFERENCE 6 (residues 1 to 507)
 AUTHORS Hu,T., Guan,T. and Gerace,L.
 TITLE Molecular and functional characterization of the p62 complex, an assembly of nuclear pore complex glycoproteins
 JOURNAL J. Cell Biol. 134 (3), 589-601 (1996)
 PUBMED [8707840](#)
 REFERENCE 7 (residues 1 to 507)
 AUTHORS Finlay,D.R., Meier,E., Bradley,P., Horecka,J. and Forbes,D.J.
 TITLE A complex of nuclear pore proteins required for pore function
 JOURNAL J. Cell Biol. 114 (1), 169-183 (1991)
 PUBMED [2050741](#)
 COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from [BC012559.1](#), [AF157322.1](#) and [BC034226.1](#).
 On Dec 5, 2002 this sequence version replaced gi:[8393858](#).

Summary: The nuclear envelope creates distinct nuclear and cytoplasmic compartments in eukaryotic cells. It consists of two concentric membranes perforated by nuclear pores, large protein complexes that form aqueous channels to regulate the flow of macromolecules between the nucleus and the cytoplasm. These complexes are composed of at least 100 different polypeptide subunits, many of which belong to the nucleoporin family. This gene encodes a member of the phe-gly (FG) repeat-containing nucleoporin subset.

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ORIGIN

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Range: from **begin** to **end** Features:

1: [CAD97957](#). Reports hypothetical prot...[gi:31874087]

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LOCUS CAD97957 291 aa linear PRI 17-JUN-2003
 DEFINITION hypothetical protein [Homo sapiens].
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 VERSION CAD97957.1 GI:31874087
 DBSOURCE embl accession [BX538002.1](#)
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 SOURCE Homo sapiens (human)
 ORGANISM [Homo sapiens](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 291)
 AUTHORS Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
 Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
 Wiemann,S.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
 Neuherberg, GERMANY
 COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by EMBL (European Molecular Biology Laboratories,
 Heidelberg/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 This clone (DKFZp686B1269) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
 information about the clone and the sequencing project is available
 at <http://mips.gsf.de/proj/cDNA/>.
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/db_xref="GOA:Q7Z3B4"
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/db_xref="UniProtKB/Swiss-Prot:Q7Z3B4"

ORIGIN

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121 pagvdpiiwe qakvdnpdse klipvpmvgf kellrrlkvq dqmtkqhqr ldvlikqeiq
181 rksgyaiqad eeqlrvqltd iqgelnaptq fkgrlnelms qirmqnhfga vrseeryyid
241 adllreikqh lkqqqgeglsh lisiikddle diklvehgln etihirggvf g

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Last update: Thu, 03 Jul 2008 Rev. 132917



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 300.000 wordsize: 3 Filter View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

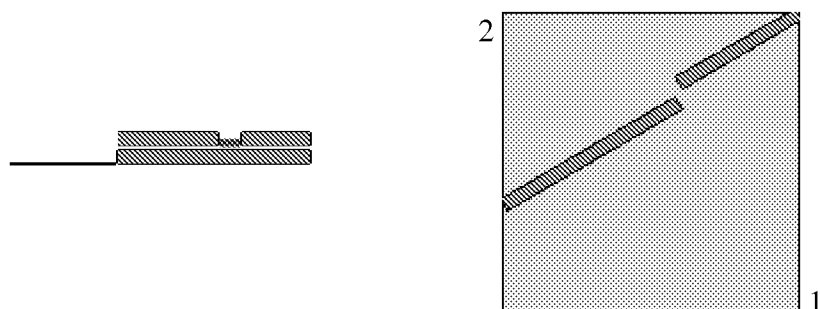
Show CDS translation Align

Sequence 1: [gil31874087|hypothetical protein \[Homo sapiens\]](#)

Length = 291 (1 .. 291)

Sequence 2: [gil1537070|nucleoporin p54 \[Rattus norvegicus\]](#) >[gil8393855|ref|NP_059057.1| nucleoporin 54kDa \[Rattus norvegicus\]](#) >[gil38257803|sp|P70582|NUP54 RAT Nucleoporin p54 \(54 kDa nucleoporin\)](#) >[gil50927635|gb|AAH78858.1| Nucleoporin 54 \[Rattus norvegicus\]](#) >[gil149033843|gb|EDL88639.1| nucleoporin 54 \[Rattus norvegicus\]](#)

Length = 510 (1 .. 510)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 538 bits (1387), Expect = 2e-151

Identities = 281/326 (86%), Positives = 288/326 (88%), Gaps = 36/326 (11%)

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Sbjct	244	VIYIVERSPNGTSRRVPATTLYAHFEQANIKTQLQQLGVTLSMTRTELSPAQIKQLLQNP	303
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CPU time: 0.04 user secs. 0.03 sys. secs 0.07 total secs.